

Run on: September 4, 2002, 16:15:58 ; Search time 172.18 Seconds
 (without alignments)
 221.041 Million cell updates/sec

OM protein - protein search, using sw model

copyright (c) 1993 - 2000 Compugen Ltd.

GenCore version 4.5

Title: US-09-052-089A-3

Perfect score: 1006

Sequence: RTIINKLFFDIAQEEENVLD.....DQSADKEMSLKKKLTMLQ 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPREMBL_19;*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1066	100	469	000467
2	1046	98	469	000467 homo sapien
3	919	86	470	000467 homo sapien
4	919	86	470	000467 homo sapien
5	654	61	4	000467 homo sapien
6	530	49	7	000467 homo sapien
7	178	43	3	000467 homo sapien
8	167	15	7	000467 homo sapien
9	167	15	7	000467 homo sapien
10	167	15	7	000467 homo sapien
11	165	15	5	000467 homo sapien
12	165	15	5	000467 homo sapien
13	165	15	5	000467 homo sapien
14	164	15	4	000467 homo sapien
15	164	15	4	000467 homo sapien
16	164	15	4	000467 homo sapien

ALIGNMENTS

RESULT ID	1	PRELIMINARY;	PRT;	469 AA.
000467		000467;		
AC		000467;		
DT	01-JUL-1997	(T-EMBLrel. 04, Created)		
DT	01-JUL-1997	(T-EMBLrel. 04, Last sequence update)		
DT	01-DEC-2001	(T-EMBLrel. 19, Last annotation update)		
DE	HTRIP.			
GN	OS	Homo sapiens (Human).		
OC	OC	Bukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	OC	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.		
NCBI-TaxID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97258620; PubMed=9104814;			
RA	Lee S.Y., Lee S.Y., Choi Y.;			
RT	"TRAF-interacting protein (TRIP): a novel component of the tumor necrosis factor receptor (TNFR)- and CD30-TRAF signaling complexes that inhibits TRAF2-mediated NF- κ B activation.";			
RT	J. Exp. Med. 185:1275-1285(1997).			
RL	CC - I - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.			
DR	EMBL: U77445; AAB2933.1; -.			
DR	InterPro: IPR01841; Znf_fing.			
DR	PFam: PF00097; zf-C3HC4; 1.			
DR	SMART: SM00184; RING; 1.			
DR	ZINC-finger.			
SO	SEQUENCE 469 AA; 53138 MW; 2D54ED04BB4ABAEC CRC64;			
Querry Match	100.0%; Score 1066; DB 4;			
Best Local Similarity	100.0%; Pred. No. 1..1e-52;			
Matches	220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 RTIINKLFFDIAQEEENVLDREFLKNELDNVRAQLSOKDKEKRSQIVDITRDTEERN 60			
Db	56 RTIINKLFFDIAQEEENVLDREFLKNELDNVRAQLSOKDKEKRSQIVDITRDTEERN 115			
QY	61 ATVVSQQLGKAEMICSTLRKQMKYLEQQDETKAQEEAGRLRSKMTMQIELLIQS 120			

			RP	SEQUENCE FROM N.A.
			RC	STRAIN=C57BL/6J; TISSUE=EMBRYO;
			RX	MEDLINE=2108650; PUBMED=11217851;
Qy	121	OLPEVEEMIRDMGYGQOSAVEQLAVYCYSVKKEYNLKEARKASGEVADKLKDFFSRK	180	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Db	176	OLPEVEEMIRDMGYGQOSAVEQLAVYCYSVKKEYNLKEARKASGEVADKLKDFFSRK	235	Aarakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Qy	181	LQTIVSELDOAKLELSAQDKEIMSLKKLTMLQ	220	Alzava K., Izawa M., Niizaki K., Kirosawa H., Kondo S., Yamana K.,
Db	236	LQTIVSELDOAKLELSAQDKEIMSLKKLTMLQ	275	Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RESULT	2		RA	Kadota K., Matsuda H.A., Ashburner M., Batatov S., Casavant T.,
ID	Q9BWF2	PRELIMINARY;	DT	Fleischmann W., Gaasterland T., Gissi C., King B., Kohwiya H.,
AC	Q9BWF2;	PRT;	DE	Kuehl P., Lewis S., Matsuo Y., Niikido T., Pesole G., Quackenbush J.,
DT	01-JUN-2001 ("REMBrel. 17, Created)		OC	Schrinl L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
DT	01-JUN-2001 ("REMBrel. 17, Last sequence update)		OX	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
DR	01-DEC-2001 ("REMBrel. 19, Last annotation update)		RN	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
DR	TRAFF INTERACTING PROTEIN.		RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M.,
DE	Homo sapiens (Human).		RA	Gustincich S., Hill D., Hoffman M., Hume D.A., Kamiya M., Lee N.H.,
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
NCBI-TaxID=10090;	[1]		RA	Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RN	{1}		RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RP	SEQUENCE FROM N.A.		RA	Hayashizaki Y.,
RC	TISSUE=LUNG CARCINOMA;		RT	"Functional annotation of a full-length mouse cDNA collection.";
RA	Strausberg R.;		CC	NCBI-TaxID=9606;
RL	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.		CC	DR
DR	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.		DR	EMBL; AK012948; BAB28567.1; -.
DR	EMBL; BC000310; AAH00310.1; -.		DR	EMBL; AK012786; BAB28469.1; -.
DR	InterPro; IPR001841; Znf_fing.		DR	MGI; MGI:1096377; Traip.
DR	Pfam; PF00097; zf-CCHC4; 1.		DR	Interpro; IPR001841; Znf_fing.
DR	SMART; SM00184; RING; 1.		DR	PFam; PF00097; zf-CCHC4; 1.
DR	Zinc-finger.		DR	Nature 405:685-690(2001).
KW	Zinc-finger.		DR	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
SQ	SEQUENCE 469 AA; 53294 MW; B9ERF3808FBC5985B CRC64;		DR	EMBL; AK012948; BAB28567.1; -.
Query Match	98.1%; Score 1046; DB 4; Length 469;		DR	EMBL; AK012786; BAB28469.1; -.
Best Local Similarity	98.6%; Pred. No. 1.4e-51;		DR	MGI; MGI:1096377; Traip.
Matches	217; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		DR	Interpro; IPR001841; Znf_fing.
Qy	1 RTIINKLFELDAQEENENVLDREFLKNEFLNVRQLSOKREKRSQVIDTDLRTEERN 60		DR	PFam; PF00097; zf-CCHC4; 1.
Db	56 RTIINKLFELDAQEENENVLDREFLKNEFLNVRQLSOKREKRSQVIDTDLRTEERN 115		DR	Nature 405:685-690(2001).
Qy	61 ATWSLQQALGKAEMLCSTLKKQMKYLEQQDETQKAOQEAGRLRSKMTMEOELLQS 120		DR	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
Db	116 ATWSLQQALGKAEMLCSTLKKQMKYLEQQDETQKAOQEAGRLRSKMTMEOELLQS 175		DR	EMBL; AK012948; BAB28567.1; -.
Qy	121 OLPEVEEMIRDMGYGQOSAVEQLAVYCYSVKKEYNLKEARKASGEVADKLKDFFSRK 180		DR	EMBL; AK012786; BAB28469.1; -.
Db	176 OREPVEEMIRDMGYGQOSAVEQLAVYCYSVKKEYNLKEARKASGEVADKLKDFFSRK 235		DR	MGI; MGI:1096377; Traip.
Qy	181 LQTIVSELDOAKLELSAQDKEIMSLKKLTMLQ 220		DR	Interpro; IPR001841; Znf_fing.
Db	236 LQTIVSELDOAKLELSAQDKEIMSLKKLTMLQ 275		DR	PFam; PF00097; zf-CCHC4; 1.
RESULT	3		Query Match	86.2%; Score 919; DB 11; Length 470;
ID	09CPB4	PRELIMINARY;	Best Local Similarity	85.5%; Pred. No. 1.9e-44;
AC	09CPB4;	PRT;	Matches	188; Conservative 19; Mismatches 13; Indels 0; Gaps 0;
DT	01-JUN-2001 ("REMBrel. 17, Created)		Qy	1 RTIINKLFELDAQEENENVLDREFLKNEFLNVRQLSOKREKRSQVIDTDLRTEERN 60
DT	01-JUN-2001 ("REMBrel. 17, last sequence update)		Db	56 RTIINKLFELDAQEENENVLDREFLKNEFLNVRQLSOKREKRSQVIDTDLRTEERN 115
DT	01-DEC-2001 ("REMBrel. 19, Last annotation update)		Qy	61 ATWSLQQALGKAEMLCSTLKKQMKYLEQQDETQKAOQEAGRLRSKMTMEOELLQS 120
DE	TRAFF-INTERACTING PROTEIN.		Db	116 ATWSLQQALGKAEMLCSTLKKQMKYLEQQDETQKAOQEAGRLRSKMTMEOELLQS 175
OS	Mus musculus (Mouse).		Qy	121 OLPEVEEMIRDMGYGQOSAVEQLAVYCYSVKKEYNLKEARKASGEVADKLKDFFSRK 180
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		Db	176 OREPVEEMIRDMGYGQOSAVEQLAVYCYSVKKEYNLKEARKASGEVADKLKDFFSRK 235
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		DR	Interpro; IPR001841; Znf_fing.
NCBI-TaxID=10090;	[1]		DR	PFam; PF00097; zf-CCHC4; 1.
RN	{1}		DR	Nature 405:685-690(2001).
RP	SEQUENCE FROM N.A.		DR	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
RX	MEDLINE=9725820; PubMed=9104814;		DR	EMBL; AK012948; BAB28567.1; -.
RA	Lee S.Y., Lee S.Y., Choi Y.;		DR	EMBL; AK012786; BAB28469.1; -.
RT	"TRAF-interacting protein (TRIP): a novel component of the tumor		DR	MGI; MGI:1096377; Traip.

DR InterPro; IPR001637; Gln_Adenylytn.
 DR InterPro; IPR000048; IQ.
 DR InterPro; IPR001609; myosin_head.
 DR InterPro; IPR004009; Myosin_N.
 DR InterPro; IPR02928; Myosin_tail.
 DR InterPro; IPR000533; tropomyosin.
 DR Pfam; PF00612; IQ; 2.
 DR Pfam; PF00063; myosin_head; 1.
 DR Pfam; PF02736; Myosin_N; 1.
 DR Pfam; PF01576; Myosin_tall; 1.
 DR Prints; PRO0193; MYOSINHEAVY.
 DR Prints; PRO0194; TROPOMYOSIN.
 DR Prodrom; P000155; myosin_head; 1.
 DR SMART; SMO015; IQ; 1.
 DR SMART; SMO0242; MYSC; 1.
 DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 DR PROSITE; PS00182; GINA_ADENYLATION; UNKNOWN_1.
 DR PROSITE; PS50056; IQ; 1.
 SQ SEQUENCE 1958 AA; 224857 MW; 3FE254327DFB9524 CRC64;

Query Match 16.7%; Score 178; DB 5; Length 1958;
 Best Local Similarity 22.7%; Pred. No. 0.027; Mismatches 58; Conservative 50; Indels 38; Gaps 7; Matches 54; Conservative 59; Mismatches 93; Gaps 6;

Qy 5 NKLFFDIAQEEENVLREFLKNEFLDNVRQLSQDKKEKRS-----QVIDLRL 53
 Db 878 NDLFLOLQTBDLSLDAEAEKVSKYKLUKNQAKMDESRIKELEDHLEEDASAGLEKKM 937
 Qy 54 DTLEERNATVVSQQLGKAEMCLSTKKQMKYEQQDDETKQAOQEAGRLRSKMTMQ 113
 Db 938 GEIELLKDVVDLESSLQAEQEKADQKVL---QDQIAQRBEEMKKMKKEKAAD 994
 Qy 114 IELLIQSQLPVEEMIRDQMVGSQVAEQLAVYCVSILKKEYENLARKASGEVADLKR 173
 Db 995 LQKTEESLOQEEEEKVKLNKAALKLQ-----TIDEMEENLSEREQVKRADV-EKV 1047
 Qy 174 LFSSRSKLQTVYSELQDQAKLE---LKSQKDQSADKEI-----MSLUKKLTMLQ 220
 Db 1048 IETELKOTQEVDDLERVKRELLEEQLKRKEMELSNASSKIEDESGLVIAQLOKIKELQ 1105

RESULT 9
 Q9UIK7 PRELIMINARY; PRT; 948 AA.

ID Q9UIK7 PRELIMINARY; PRT; 948 AA.
 AC Q9UIK7; PRELIMINARY; PRT; 948 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)

DE ELKS.

GN ELKS.

OS Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Buterilia; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Nakata T.;

RT "Fusion of a Novel Gene, ELKS, to c-ret in a Papillary Thyroid

RT Carcinoma,"

RR Submitted (JUN 1998) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AB015617; BAA88763; 1; -

DR InterPro; IPR02017; Spectrin.

SQ SEQUENCE 948 AA; 108792 MW; 344297FD9C97602 CRC64;

Query Match 15.7%; Score 167; DB 4; Length 948;
 Best Local Similarity 24.2%; Pred. No. 0.055; Mismatches 58; Conservative 50; Indels 38; Gaps 7; Matches 58; Conservative 50; Mismatches 94; Gaps 38; Indels 38; Gaps 7;

Qy 6 KLFEDIAQEEENVLREFLKNEFLDNVRQLSQDKKEKRSQVIDLRLTLEERNATV 65
 Db 535 KDMLDVKERKVNLQK-----KIEHQDKEKOMSISLKVRSLOADTTNTDTALT 589
 Qy 66 LQQLGKAEMCLSTKKQMKYEQQDDETKQAOQEAGRLRSKMTMQEELLQSQLPV 125
 Db 599 LEEALAEKERTIERLK-----EORDREREKQEDIDNYKKDLKELKEVSKLQGDLSK 643
 Qy 126 EEMIRDMGVQGS-----AVEQLAVYCV---SLKKEVNLEKARKAS 163
 Db 644 EASLDLKEHASSLASSGLKKSRLKTLEAQKEKQEEOLKMSQKKHAKEAR-AS 702
 Qy 164 GEVAK---LRKDIPSSRSKLQTVYSELQDQAKLESAKDSLQADKEMSLKRLTMQ 220
 Db 703 PEMSDRQHLEIRETRYKDESSKAQEVDRLLIEKEVENEKNDDKKIAEL-ESLTSRQ 761

RESULT 10
 Q9Q84 PRELIMINARY; PRT; 2473 AA.

ID Q9Q84 PRELIMINARY; PRT; 2473 AA.
 AC Q9Q84; PRELIMINARY; PRT; 2473 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)

DE LEKI (FRAGMENT).

Query Match 15.7%; Score 167; DB 4; Length 529;

GN 6520404A22RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurogathi; Muridae; Murinae; Mus.
 NCBI_TAXID=10090;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=99305627; PubMed=10373470;
 RA Goodwin R.L., Paben-Pena L.M., Foster G.C., Bader D.;
 RT "The cloning and analysis of LEK1 identifies variations in the
 LEK1/centromere protein F/miosin gene family.";
 RL J. Biol. Chem. 274:18597-18604 (1999).
 DR EMBL; AF194970; AF071961;
 MGD; MGI:1915046; 6530404A22RIK.
 FT NON_TER 1
 SEQUENCE 2473 AA; 281903 MW; 504E91A1A150A3E5 CRC64;

Query Match 15.7%; Score 167; DB 11; Length 2473;
 Best Local Similarity 23.8%; Pred. No. 0.14; Indels 44; Gaps 5;
 Matches 58; Conservative 54; Mismatches 88; Incls 44; Gaps 5;

QY 10 DLQEQQEN---WLDREFLKDNEQDNVRQLSOKDKEKRDSQVITDLRDTLEARNVVS 65
 Db 1638 ELERSEEMQELAIDSENKAENETIKAQDEMKSLRIFELDULTVTEREALAKQOE 1697
 QY 66 LQALGKAEMCSTLKKOMYKSGO-----ODITKQAOEAGRLRSKMT 110
 Db 1698 KQSVRSELDERCCSSLRLLEKEQARVQMEEDSKSAMLMLOMQLKELREVAALCNDQET 1757
 QY 111 MEQFELLIQSQPEVEEMTRDMGVGQSAVEQAVCVSLKKEENLKEARKASGEVADKL 170
 Db 1758 LKAOEQSLSQDOPGEEVHHL-----KSSTRKVHIDAKEKHONILBOLKESKHADIL 1810
 QY 171 R-----KDLF-----SSRSKIQIVSSELDAKLEKSAQKDLQSAKDEKMSL 212
 Db 1811 KDRVENLCEGLILESEKKNMFQAEKSKEIQTLLSEIQRMAQNQDQLELISTRSENEML 1870
 QY 213 KKKL 216
 Db 1871 IKEL 1874

RN RESULT 11
 090338 PRELIMINARY; PRT; 1092 AA.
 AC 090338
 DT 01-Nov-1996 (TREMBlrel. 01, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE MYOSIN HEAVY CHAIN (FRAGMENT)
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Neodiplopoda; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 NCBI_TAXID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV_NIPPONBARE;
 RA Bueill C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Burr P.C.,
 RA Hsiao J.J., Zisman V., Pali G., Bowman C.L., Fujii C.Y., VanAken S.E.,
 RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblum T.V.,
 RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
 RT "Oriza sativa chromosome 10 BAC OSJNB00010.4 genomic sequence.";
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC025783; AAC20041.1; -
 SQ SEQUENCE 1578 AA; 178947 MW; CB7E1DB68A821A0 CRC64;

Query Match 15.5%; Score 165; DB 10; Length 1578;
 Best Local Similarity 25.7%; Pred. No. 0.12; Indels 32; Gaps 6;
 Matches 59; Conservative 48; Mismatches 91; Incls 32; Gaps 6;

QY 4 INKLFEDLQEEQENYLDRFLKNEDNVVAQLSOKDKEKR-----SSQVITDLRDTL 55
 Db 777 ISKL-----EHENVELSER-----ISGLSQTLYANEELSMQMDSSRLTSLNLKBL 826
 QY 57 EERNATVVSQQLGKAEMCSTLKKOMYKLEQODETKQAEQEEAGRLSKMT-TMEGIE 115
 Db 827 EOEVAKVLKLMDERSRSUUTNLKDELQVEAKVELKLQMDSSRLTSLNLKDELQVE 886
 QY 116 -----ILQSQLPVNE---MIRDGMVGQSAVEQAVCVSISKEYENLKEARK 161
 Db 887 AQKVELKENQOLESHRLSVEQDESEALRSNAQATDVHVERCKSQTQTLTADLIKOKL 946
 QY 162 ASGEVADKRLKDLSSRSRKTQVYSELDAKLEKSAQKDLQSAKDEKMSL 211
 Db 947 EVHGVASHEQELEQSKRTMDFTKLESLAKLSSLQBDISLKEQSIIS 996

SQ SEQUENCE 1092 AA; 125885 MW; B6BABBA3963BEEBA CRC64;

RESULT 17

RESULT 17

RESULT	099M12	PRELIMINARY;	PRT;	976 AA.
ID	099M12;			
AC	099M12;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	RAB6-INTERACTING PROTEIN 2 ISOFORM A.			
DR	Mus musculus (Mouse);			
DR	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
DR	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
DR	NCBI_TAXID=1090;			
DR	[1]			
RP	SEQUENCE FROM N.A.			
RA	Monier S., Janoueix-Lerosey I., Jollivet F., Goud B.;			
RA	"Characterization of a novel interaction partner of the small GTPase Rab6";			
RA	Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL: AF340029; AAK63824; -;			
DR	INSPRO: IPR02017; Specinr.			
DR	PRINTS; PRO0194; TROPOMYOSIN.			
SQ	SEQUENCE: 976 AA; 111931 MW; 48731867C8D8CD6F CRC64;			
	Quarry Match	15.2%	Score	162; DB 11; Length 976;
	Best Local Similarity	24.2%	Pred.	No. 0..11; Mismatches 58; Conservative 48; MisMatches 96; Indels 38; Gaps
OY	6 KLFDFLQAEEENVLDDEFLKNELDNVRAQLSQDKERKDSQVITDLNTLEERNATVWS 65			
Db	563 KDMGLVKERYKVNVLOK----KLENQOLQRDKERKMSLKERVKSLQADTTNHDALTq 617			
Oy	66 LQQLGKAEMLCSTLKKQMKYLEQQQDETQKQAEAGRLRSKMTMEQIELLIQSQLPVE 125			
Db	618 LEEALADAKERTERLKR----EQRDRERKEQEDITYKKDLKDRKKVSLQGDLSSEK 671			
OY	126 EEMIRQVGQS-----AWEQAVYCV---SLKKEYENLKARKAS 163			
Db	672 EASLDIKEHASSLASSGLKKSRLKILEALEQKKECLKMQESQLKKHAATELEAR AS 730			
OY	164 GEVADK---LKDFFSSRSKQTYWVSYLDOAKLELKRAOKDQOSADEKIMSLLKLTMQ 220			
Db	731 PEMSDRQQLREISRYKDESSSKAQTEVDRLBILKEVENEKNDDKKIAEL-ESLTSRQ 7889			
RESULT	19			
099M11				
099M11	PRELIMINARY;	PRT;	1120 AA.	
AC	099M11;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	RAB6-INTERACTING PROTEIN 2 ISOFORM B.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TAXID=1090;			
RP	SEQUENCE FROM N.A.			
RA	Monier S., Janoueix-Lerosey I., Jollivet F., Goud B.;			
RA	"Characterization of a novel interaction partner of the small GTPase Rab6";			
RA	Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL: AF340029; AAK63824; -;			
DR	INSPRO: IPR02017; Specinr.			
SEQUENCE	1120 AA; 128330 MW; A542B526FAEDF9C7 CRC64;			

QY	6	KLFFDLAQEEENVLREFKNELDNVRAQLSOKDKKEKRDSQVIIIDLTDT
Db	563	KDMDVYKERVNLUOK---K-KIENQOLRDKEQKMSLKVRSQADD
QY	66	LQQALGKAGEMCSTLKKQMKYLEQQDDETKOQAQEAGRLRSKMTMQEIE
Db	618	LLEEALADKERTIERLK-----EQRDRERKQEEDTYKKDLRKLREKV
OY	126	EEMFRDMGCGOS-----A-VEOLAVYC-V---SLRKKEY
Db	672	EASLIDLKEHASSLASSGLKKSRSRKTLEALEQKKECLKMSOLQKKAH
QY	164	GEVADK---LRKDLESSRSKQTVSELQAKLELSAQKLOSAKDEIMM
Db	731	PEMSDRIOQLEIREISRYKEDDESSSKAQTEVDRILLELKVEVENEKNDDKKAIA
RESULT	20	
09063		
ID	096663	PRELIMINARY; PRT: 1743 AA.
AC	096663;	
DT	01-MAY-1999	(TREMBLrel: 10, Created)
DT	01-MAY-1999	(TREMBLrel: 10, last sequence update)
DT	01-DEC-2001	(TREMBLrel: 19, last annotation update)
DE	MYOSIN HEAVY CHAIN (FRAGMENT).	
GN	DJMC-B.	
OC	Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Serialia	
OC	Dugesia Japonica (Planarian).	
OS	Dugesia; Japonica (Planarian).	
OX	NCBI_TaxID=6101;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Kobayashi C., Agata K., Orii H.;	
RL	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RA	Kobayashi C., Kobayashi S., Orii H., Agata K., Watnabe	
RT	"Identification of two distinct muscles in the planarian	
RT	Japonica, by the expression of myosin heavy chain genes	
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases	
CC	- - SIMILARITY: BELONGS TO THE GNTR FAMILY OF TRANSCRIPTION REGULATORS.	
DR	EMBL: AB015485; BAA34955.1; -.	
DR	HSSP; P08799; 1MND.	
DR	InterPro; IPR01064; Crystallin.	
DR	InterPro; IPR01637; GlnP_Adenylyln.	
DR	InterPro; IPR00524; HTH_GntR.	
DR	InterPro; IPR00048; IQ.	
DR	InterPro; IPR01609; myosin_head.	
DR	InterPro; IPR02928; Myosin_tail.	
DR	InterPro; IPR00533; Tropomyosin.	
DR	Pfam; PF00612; IQ; 2.	
DR	Pfam; PF00063; myosin_head; 1.	
DR	Pfam; PF01576; Myosin_tail; 1.	
DR	PRINTS; PR0005; RPHGNTR.	
DR	PRINTS; PR00193; MYOSINHEAVY.	
DR	PRINTS; PR00194; TROPOMYOSIN.	
DR	PRODOM; PD00055; myosin_head; 1.	
DR	SMART; SM00015; IQ; 1.	
DR	SMART; SM00242; MSc; 1.	
DR	PROSITE; PS0025; CRYSTALLIN_BETA(GAMMA); UNKNOWN_1.	
DR	PROSITE; PS00182; GLNA_ADENYLATION; UNKNOWN_1.	
DR	PROSITE; PS50096; IQ; 1.	
KW	DNA-binding; Transcription regulation.	
NON_TER	1	
SEQUENCE	1743 AA:	200417 MW: 004A821FA6CF7C2 CRC64

DR PRINTS; PR00194; TROPOMYOSIN
 DR PRODOM; PD000355; myosin_head; 1.
 DR SMART; SM00015; ID; 1.
 DR PROSITE; PS50096; IQ; 1.
 FT NON_TER 1 1
 SEQUENCE 1219 AA; 141202 MW; BAC6P574DA4AFBBB CRC64;

Query Match 15.1%; Score 160.5; DB 5; Length 1219;
 Best Local Similarity 28.1%; Pred. No. 0.16; Mismatches 56; Conservative 46; Indels 27; Gaps 7; Matches 58; Mismatches 7; Conservatve 54; Indels 53; Gaps 7;

Qy 10 DLRAQEENVLDRFLKNEEL-N-DNTR--AQLSQDKKEKRDQSQVITDITRDLERNAV 65
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 336 DLKSTOENVEDLRRVKRELEENTRKEAIISSNLKDEONIUSOLQRKIKELQLEE 395

Qy 66 LQDQALGKAEMLCSTLKKOMKYLEQQDETQQAEGRLRSKMTMEQTELLIQSQLPEV 125
 |:| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 396 LEEELAERNARAKVEKORAEELNRELEELGERIDEAGG---ATSAQIELNKKRE-AEL 449
 |:| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Qy 126 EEMTRDMGVGOSAVEOLAVCVSIRKEYNLPARKASGEVAEPLRKLFSSSKLQTY 185
 |:| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 450 LKTRRDL---E-EASLQHEAQISALRKHHOD-----AANEMADQV-----DOLQKV 492
 RP

Qy 186 SELDQAKLELKSKQDKLQS 204
 |:| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 493 SKLKDQDKDILKREMDLES 511

RESULT 26

ID 061043 PRELIMINARY; PRT; 2168 AA.
 AC 061043; TREPMBrel. 01, Created)
 DT 01-NOV-1996 (TREPMBrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREPMBrel. 19, Last annotation update)
 DE NINEIN.
 GN NIN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RA Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 SEQUENCE FROM N.A.

RP STRAIN=C37BL/6;
 RC Boulton-Castaing V., Moudjou M., Ferguson D.J.P., Mucklow M.,
 RA Belkaid Y., Milon G., Crocker P.R.;
 RT "Molecular characterisation of ninein, a new coiled-coil protein of
 the centrosome"; J. Cell Sci. 108: 0-0(1996).
 RL EMBL; U040342; AAA82341; -.
 DR MGD; MGI:105108; NIN.
 DR InterPro; IPR002048; EF-hand
 SEQUENCE 2168 AA; 241668 MW; FDB0EC0F240E58E7 CRC64;

Query Match 15.0%; Score 160; DB 5; Length 435;
 Best Local Similarity 24.5%; Pred. No. 0.064; Mismatches 56; Conservative 58; Indels 22; Gaps 6; Matches 58; Mismatches 93; Conservatve 54; Indels 53; Gaps 7;

Qy 4 INKLFLFDLRAQEENVLDRFLKNEEL-N-DNTR--AQLSQDKKEKRDQSQVITDITRDLERNAV 63
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 55 IFRVYFLNANDLVDVSDLSQEDDNALMSMKAYEVKRNKEPKDQIRDKEKOKCLKT 114

Query Match 15.0%; Score 160; DB 5; Length 435;
 Best Local Similarity 24.5%; Pred. No. 0.064; Mismatches 56; Conservative 58; Indels 22; Gaps 6; Matches 58; Mismatches 93; Conservatve 54; Indels 53; Gaps 7;

Qy 64 VSLOQALGKAEMLCSTLKKOMKYLEQQDETQQAEGRLRSKMTMEQTELLIQSQLPEV 125
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 115 AGLEQKVQKDFLISSYVYEQIVLKSDAHVDGLRKENKLTKSQIISMGISAIALAGSA 174

Qy 124 EVEEMTRDMGVGOSAVEOLAVCVSIRKEYNLPARKASGEVAEPLRKLFSSSKLQTY 179
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 175 DADRLLKN---EADPHVJANWVSTKRELRCESKTELRLNNVVVKVQNDLRKEELKR- 229

Qy 180 KLTQWYSELQ---QAKL--EUKSAQDKLQS---DKEIMSLLKK 215
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 230 KLEERYVSHLSDLYQAOEKQIAFENKTAVIDSPWASCGLNNSNIALKRE 278

RESULT 28

Q9NJ22 PRELIMINARY; PRT; 1229 AA.
 ID Q9NJ22
 AC Q9NJ22
 DT 01-OCT-2000 (TREPMBrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREPMBrel. 15, Last sequence update)
 DE MYOSIN HEAVY CHAIN CATCH (SMOOTH) MUSCLE SPECIFIC ISOFORM (FRAGMENT).
 DE DE
 GN MHC
 OS Aequipecten irradians (Bay scallop).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;
 OC Pectinoidea; Pectinidae; Argopecten.
 OX NCBI_TaxID=31199;
 RN [1]
 SEQUENCE FROM N.A.

RP MEDLINE=20090924; PubMed=10623517;

Qy 115 ELLQSQLPQEVEEMTR--DMGVGOSAVEOLAVCVSIRKEYNLPARKASGEVAEPLRKLFSSSKLQTY 164
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 1698 NLLKDELERIKQLHRCPDPDLQOKMSVSYLSNEKLKEKEVISEELKSCADKAESSL 1757
 RP

Qy 165 -----EVADKLKDLFSSRSKQLQTVSELDQAKLELKSAQDKLQ----- 203

RA	RT	DR	DR
"Catchin," a novel protein in molluscan catch muscles, is produced by alternative splicing from the myosin heavy chain gene.;"	"Catchin, a novel protein in molluscan catch muscles, is produced by alternative splicing from the myosin heavy chain gene.;"	SMART; SM00015; IQ; 1.	PROSITE; FS50096; IQ; 1.
J. MOL. BIOL. 295:169-178(2000).	J. MOL. BIOL. 295:169-178(2000).	NON_TER	1
EMBL; AF183909; AF062395.1; -.	EMBL; AF183909; AF062395.1; -.	SEQUENCE	1243 AA; 143531 MW; B5C7219BFF2BE8AE CRC64;
DR	DR	DR	DR
InterPro; IPR000048; IQ.	InterPro; IPR000048; IQ.	InterPro; IPR001603; myosin_head.	InterPro; IPR001603; myosin_head.
InterPro; IPR02928; Myosin_tail.	InterPro; IPR02928; Myosin_tail.	InterPro; IPR02928; Myosin_tail.	InterPro; IPR02928; Myosin_tail.
InterPro; IPR00533; Tropomyosin.	InterPro; IPR00533; Tropomyosin.	InterPro; IPR00533; Tropomyosin.	InterPro; IPR00533; Tropomyosin.
Pfam; PF00063; myosin_head; 1.	Pfam; PF00063; myosin_head; 1.	Pfam; PF00157; Myosin_tail; 1.	Pfam; PF00157; Myosin_tail; 1.
PRINTS; PR00194; Tropomyosin.	PRINTS; PR00194; Tropomyosin.	PRINTS; PR00194; Tropomyosin.	PRINTS; PR00194; Tropomyosin.
ProDom; PD00035; myosin_head; 1.	ProDom; PD00035; myosin_head; 1.	ProDom; PD00035; myosin_head; 1.	ProDom; PD00035; myosin_head; 1.
PROSITE; PS50096; IQ; 1.	PROSITE; PS50096; IQ; 1.	PROSITE; PS50096; IQ; 1.	PROSITE; PS50096; IQ; 1.
SEQUENCE	1229 AA; 142180 MW; 1764276CB904FDC9 CRC64;	SEQUENCE	1229 AA; 142180 MW; 1764276CB904FDC9 CRC64;
Query Match	15.0%; Score 159.5; DB 5; Length 1243;	Query Match	15.0%; Score 159.5; DB 5; Length 1243;
Best Local Similarity	27.4%; Pred. No. 0.19; Gaps	Best Local Similarity	27.4%; Pred. No. 0.19; Gaps
Matches	57; Conservative	Matches	57; Conservative
Db	336 DLKSTQENVDLERVKRELEENYRKEAEISSLNKLEDEQNLVSQLQKIKELQARIEE 395	Db	336 DLKSTQENVDLERVKRELEENYRKEAEISSLNKLEDEQNLVSQLQKIKELQARIEE 395
Qy	10 DLAQEENVLDREFLKLNL-DNVR--AQLSQDKERKDSQVITDLRTLEERNATVVS 65	Qy	10 DLAQEENVLDREFLKLNL-DNVR--AQLSQDKERKDSQVITDLRTLEERNATVVS 65
Db	336 DLKSTQENVDLERVKRELEENYRKEAEISSLNKLEDEQNLVSQLQKIKELQARIEE 395	Db	336 DLKSTQENVDLERVKRELEENYRKEAEISSLNKLEDEQNLVSQLQKIKELQARIEE 395
Qy	66 LQALGKAEMLCSTLKKOMYKYLEQODETKQAOEEAGRURSKMKTMEQIELLQLQPEV 125	Qy	66 LQALGKAEMLCSTLKKOMYKYLEQODETKQAOEEAGRURSKMKTMEQIELLQLQPEV 125
Db	396 LEEELAERNARAKREWKRALKRNLNRLEELGERLDEAGG----ATSQAELNKRE-AEL 449	Db	396 LEEELAERNARAKREWKRALKRNLNRLEELGERLDEAGG----ATSQAELNKRE-AEL 449
Qy	126 EEMRDGMVGQSAVQLAVCVSLKKEYENKEARKASGEVADKLRLDFSSRSRKQTVY 185	Qy	126 EEMRDGMVGQSAVQLAVCVSLKKEYENKEARKASGEVADKLRLDFSSRSRKQTVY 185
Db	450 LKIRKD--EEASLOHEADQISALARHKD-----AAANEADQV-----DQLQKV 492	Db	450 LKIRKD--EEASLOHEADQISALARHKD-----AAANEADQV-----DQLQKV 492
Qy	186 SELDQAKLKSQAQDLSADKEIMSLK 213	Qy	186 SELDQAKLKSQAQDLSADKEIMSLK 213
Db	493 SKSERKEKQOLRSEVEDLQAOIQHISKNK 520	Db	493 SKSERKEKQOLRSEVEDLQAOIQHISKNK 520
RESULT	29	RESULT	30
Q9NJ21	PRELIMINARY; PRT; 1243 AA.	Q9NJ20	PRELIMINARY; PRT; 1253 AA.
ID	Q9NJ21; 01-OCT-2000 (TREMBLrel. 15, Created)	ID	Q9NJ20; 01-OCT-2000 (TREMBLrel. 15, Created)
AC	Q9NJ21; 01-OCT-2000 (TREMBLrel. 15, Last sequence update)	AC	Q9NJ20; 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	MYOSIN HEAVY CHAIN CARDIAC MUSCLE SPECIFIC ISOFORM 1 (FRAGMENT).	DE	MYOSIN HEAVY CHAIN CARDIAC MUSCLE SPECIFIC ISOFORM 2 (FRAGMENT).
MHC	Aequipecten irradians (Bay scallop).	MHC	Aequipecten irradians (Bay scallop).
GN	Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida; OC	GN	Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida; OC
OC	Pectinoidea; Pectinidae; Argoppecten.	OC	Pectinoidea; Pectinidae; Argoppecten.
NCBI_TaxID	31199; [1]	NCBI_TaxID	31199; [1]
RN	SEQUENCE FROM N.A.	RN	SEQUENCE FROM N.A.
RX	MEDLINE-20090924; PubMed-10623517;	RX	MEDLINE-20090924; PubMed-10623517;
RA	Yamada A., Yoshio M., Oiwa K., Nyitrai L.;	RA	Yamada A., Yoshio M., Oiwa K., Nyitrai L.;
RT	"Catchin, a novel protein in molluscan catch muscles, is produced by alternative splicing from the myosin heavy chain gene.;"	RT	"Catchin, a novel protein in molluscan catch muscles, is produced by alternative splicing from the myosin heavy chain gene.;"
RL	J. Mol. Biol. 295:169-178(2000).	RL	J. Mol. Biol. 295:169-178(2000).
EMBL	AF183909; AF062395.1; -.	EMBL	AF183909; AF062395.1; -.
HSSP	P24733; IWDC.	HSSP	P24733; IWDC.
DE	InterPro; IPR000048; IQ.	DE	InterPro; IPR000048; IQ.
DR	IPR001603; myosin_head.	DR	IPR001603; myosin_head.
DR	InterPro; IPR02928; Myosin_tail.	DR	InterPro; IPR02928; Myosin_tail.
DR	InterPro; IPR002017; Spectrin.	DR	InterPro; IPR002017; Spectrin.
DR	InterPro; IPR00533; Tropomyosin.	DR	InterPro; IPR00533; Tropomyosin.
Pfam	PF00063; myosin_head; 1.	Pfam	PF00063; myosin_head; 1.
DR	PF01576; Myosin_tail; 1.	DR	PF01576; Myosin_tail; 1.
DR	PRINTS; PR00194; Tropomyosin.	DR	PRINTS; PR00194; Tropomyosin.
DR	ProDom; PD00035; myosin_head; 1.	DR	ProDom; PD00035; myosin_head; 1.
DR	SMART; SM00015; IQ; 1.	DR	SMART; SM00015; IQ; 1.
DR	PROSITE; PS50096; IQ; 1.	DR	PROSITE; PS50096; IQ; 1.
FT	NON_TER	FT	NON_TER
SQ	SEQUENCE	SQ	SEQUENCE
Qy	10 DLAQEENVLDREFLKLNL-DNVR--AQLSQDKERKDSQVITDLRTLEERNATVVS 65	Qy	10 DLAQEENVLDREFLKLNL-DNVR--AQLSQDKERKDSQVITDLRTLEERNATVVS 65
Db	336 DLKSTQENVDLERVKRELEENYRKEAEISSLNKLEDEQNLVSQLQKIKELQARIEE 395	Db	336 DLKSTQENVDLERVKRELEENYRKEAEISSLNKLEDEQNLVSQLQKIKELQARIEE 395
Qy	66 LQALGKAEMLCSTLKKOMYKYLEQODETKQAOEEAGRURSKMKTMEQIELLQLQPEV 125	Qy	66 LQALGKAEMLCSTLKKOMYKYLEQODETKQAOEEAGRURSKMKTMEQIELLQLQPEV 125

RESULT 31
 Q1042 PRELIMINARY; PRT; 1951 AA.
 AC 017042; ID 017042; DT 01-NOV-1996 (TREMBrel. 01, Created)
 DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE MYOSIN HEAVY CHAIN.
 OS Aequipecten irradians (Bay scallop).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;
 OC Pectinidae; Pectinidae; Argoppecten.
 OX NCBI-TaxID=31199;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MYOSIN, CATCH (SMOOTH) ADDUCTOR;
 RX MEDLINE=95108023; PubMed=7899102;
 RA Nyitraj L., Jancso A., Ochiai Y., Graf L., Szent-Gyorgyi A.G.;
 RT produced by alternative RNA splicing from a single gene.";
 RL PROC. NATL. ACAD. SCI. U.S.A. 91:12686-12690(1994).
 DR HSSP; P14733; IWDG;
 DR InterPro; IPR00048; IQ.
 DR InterPro; IPR01609; myosin_head.
 DR InterPro; IPR02928; myosin_tail.
 DR InterPro; IPR002017; spectrin.
 DR Pfam; PF00612; IQ; 2.
 DR Pfam; PF00063; myosin_head; 1.
 DR Pfam; PF02736; myosin_N; 1.
 DR Pfam; PF01576; myosin_tail; 1.
 DR PRINTS; PRO0193; MYOSINHEAVY.
 DR SMART; SM00015; IQ; 1.
 DR SMART; SM00242; MASC; 1.
 DR PROSITE; PS50096; IQ; 1.
 DR SEQUENCE 1951 AA; 224253 MW; 1FDC3D691C1410 CRC64;

Query Match 15 0%; Score 159 5; DB 5; Length 2139;
 Best Local Similarity 27.48%; Pred. No. 0.29%;
 Matches 57; Conservative 49; Mismatches 75; Indels 27; Gaps 7;

QY 10 DLQAEEENVLDRFLKELN-DNVR--AOLSOKKEKRDQSIVITLRTDLTEARNATIVS 65
 Db 1058 DLKSKPQENTEDLERVKRELEENVRKKEAELSSLNKLEEQNQLSQLQRKKIKELQARIEE 1117
 QY 66 LQQLGKAEMCSTIKKQMLEQODETRQAOERAGRURSKMTMEQIELLLQSQPEV 125
 Db 1118 LEEELEARNARAKVEKQRAELNRELEELGERDEBGG---ATSAQTELKKRE-AEL 1171
 QY 126 EEMIRDGMVGQSAVEQALAVCVSISKKEYENLKEARKASGEVADKRDLESSLRSKQTVY 185
 Db 1172 LKTRRDL--EEASLQEQAISRKHHOD----ANEMADQY-----DOLQKV 1214
 QY 186 SELQAAKLELKSKQDKLQSADKETMSL 213
 Db 1215 SKSEKEQDQLRSEVEDLQAOIQHISKNK 1242

RESULT 33
 Q07380 PRELIMINARY; PRT; 1790 AA.
 ID 007380; AC 007380; DT 01-NOV-1996 (TREMBrel. 01, Created)
 DT 01-JUL-1997 (TREMBrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 17, Last annotation update)
 DE HYPOTHETICAL PROTEIN YD1058W.
 GN US01 OR YD1058W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Saccharomyces cerevisiae; Ascomycota; Saccharomycotina; Saccharomycetes;

RESULT 32
 Q07569 PRELIMINARY; PRT; 2139 AA.
 ID 007569; AC 007569; DT 01-NOV-1996 (TREMBrel. 01, Created)
 DT 01-JUL-1997 (TREMBrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE MYOSIN HEAVY CHAIN.
 GN MHCA.
 OS Entamoeba histolytica.
 OC Entamoeba histolytica; Entamoebidae; Entamoeba.
 OX NCBI-TaxID=5759;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HMI:IMS;
 RX MEDLINE=93295130; PubMed=8515774;
 RA Raymond-Denise A., Sansonetti P., Guillen N.;
 RT "Identification and characterization of a myosin heavy chain gene from the human parasitic pathogen Entamoeba histolytica.",
 RL Mol. Biochem. Parasitol. 59:123-131(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HMI:IMS;
 RA Guillen N.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; L03534; RAB48065.1; -.
 DR HSSP; P08799; IMND.
 DR InterPro; IPR00048; IQ.
 DR InterPro; IPR01609; myosin_head.
 DR Pfam; PF00612; IQ; 2.
 DR Pfam; PF00063; myosin_head; 1.
 DR PRINTS; PRO0193; MYOSINHEAVY.
 DR PRODOM; FD000355; myosin_head; 1.
 DR SMART; SM00242; MASC; 1.
 DR PROSITE; PS50096; IQ; 1.
 DR SEQUENCE 2139 AA; 245225 MW; C68307341DB51DD1 CRC64;

Query Match 15 0%; Score 159 5; DB 5; Length 2139;
 Best Local Similarity 24.08%; Pred. No. 0.32%;
 Matches 60; Conservative 49; Mismatches 96; Indels 45; Gaps 7;

QY 5 NKLFFDL-AQEENNVLDRFLKELNLDLQKELDDBITKA--DW-SQYLOKQKEYESIANKMEEKEIGNDW 1200
 Db 1144 NKIEGLRNQKQTKELDDBITKA--DW-SQYLOKQKEYESIANKMEEKEIGNDW 1200
 QY 51 TLRDPLEERNATVYSLQQLGKAEMCLCSTLKKOMYLEDQODETRQAOERAGRURSKMT 110
 Db 1201 NREKTIKEKELEIOSLQEKLDTEVEKEDAEKKKEIEK--EMKALQEEKENVESSKNS 1257
 QY 111 MEQIELLQSQPEVEMIRDGMVGQSAVEQALAVCVSISKKEYENLKEARKASGEVADKL 170
 Db 1258 TEKDRLKEDNLKDQTKLDMTADENEKLUKAKADLEAQDNHERAVADELLNK 1317
 QY 171 R---KDLFSSRSKIQ-----TVSELDQAKLETKSAQDKLQA 205
 Db 1318 KAQSKELNLSKAELEALTAKSKVSEKNKDSNEKAALSEEIDAOANEKUNIQADLRKA 1377
 QY 206 DKEIMSLKK 215
 Db 1378 TADLOEANER 1387

OX NCBI_TAXID=4932;
 RN {1}
 SEQUENCE FROM N_A.
 RA Blocker H.; Brandt P.; to the EMBL/GenBank/DDBJ databases.
 RL Submitted (JUL-1996) ;
 DR EMBL; Z74105; CAA98211; 1; -;
 DR SGD; S002216; US01.
 DR InterPro; IPR002117; Spectrin.
 SQ SEQUENCE 1790 AA; 206450 MW; 90062544F55A52EE CRC64;

Query Match 14.9%; Score 159; DB 3; Length 1790;
 Best Local Similarity 23.7%; Pred. No. 0.29; Gaps 7;
 Matches 55; Conservative 48; Mismatches 80; Indels 44; Gaps 7;

QY 1 RTIINKLFFDIAQ--EENVLDRFLK-----NELDNVRQLSQDKKEKRDQSQT 48
 Db 1369 RKLNEGSSITQESEKINWLEDILRQNENEKAKEDNTREL-EKVLSDND--- 1423
 QY 49 IDTLRQTLERBRNATVYSLQQL-----GKAEMLCSTLKQMYLEQODDETQAOEE 100
 Db 1424 ---ELLEEKONTIKSLODEILSYKDTRNEKLSITERDKRDLLESKELRAOES 1478

QY 101 AGRLASMKMUTMEQIELLQLSQLPVEEMIRDGMVGQSAVE---QLVAVCVSLKEYENL 156
 Db 1479 KAKVERGLKLEESSKEELSKEMMRL--ESTISNETELKSSMETIRKSDEKL 1535
 QY 157 KEARKASGEVADKL-----KDFLSSRSKLTQTVY---SELDQAKELSAQ 199

Db 1536 EQSKKSAEEDIKLNQHEKDSLISRINESERDEELJKSLRIEAKSGSELETVKQBLNNAQ 1595
 QY 200 KDLQSADEKLMSSKRL 216
 Db 1596 EKIRINAENTVLSKRL 1612

RESULT 34
 09TV61 PRELIMINARY; PRT; 1939 AA.

ID 09TV61; AC 09TV61;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MYOSIN HEAVY CHAIN 2X.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N_A.
 RC STRAIN=LANDRACE; TISSUE=SKELETAL MUSCLE;
 RA Chikuni K., Tanabe R., Muroya S., Nakajima I.;
 RT Differences in molecular structure among the porcine myosin heavy chain-2a, -2x, and -2b isoforms.;
 RT Meat Sci 57:31-37(2001);
 DR EMBL; AB025262; BAM82146.1; -.
 DR HSSP; P13538; 2MYS.
 DR InterPro; IPR000048; IQ.
 DR InterPro; IPR001609; myosin_head.
 DR PRINTS; PR0019; MO5INHBAVY.
 DR InterPro; IPR002928; Myosin_tail.
 DR InterPro; IPR002017; Spectrin.
 DR Pfam; PF00612; IO: 2.
 DR Pfam; PF0063; myosin_head; 1.
 DR Pfam; PF02736; Myosin_N; 1.
 DR InterPro; IPR004009; Myosin_N.
 DR InterPro; IPR002928; Myosin_tail.
 DR SMART; SM00015; IO: 1.
 DR SMART; SM00242; MYSC; 1.
 DR PROSITE; PS50056; IO: 1.
 SQ SEQUENCE 1941 AA; 223243 MW; E2AD1637FFDBB8127 CRC64;

Query Match 14.9%; Score 158.5; DB 5; Length 1941;
 Best Local Similarity 27.5%; Pred. No. 0.33; Gaps 7;
 Matches 56; Conservative 49; Mismatches 72; Indels 27; Gaps 7;

QY 5 NKLFFDLAQEEENVLDREFKNL-DNVR--AOLSOKKEKRDQSQTDTLROTLER 60
 Db 1053 SKVEDDLKSPQYENNTEDLERVKRELEENVIRKEAEELTTLNSKLEDEQNLSQLRKIKEQ 1112
 QY 61 ATVVLSQLQALGKAEMLCSTLKQMYLEQODDETQAOAEGRURSKMTIMEQTELLIQS 120
 Db 1113 ARIEELEELAERNARSKVEKQRAELNBLEELGERLDEAGG---ATSAQIELNKKR 1167

QY 121 OLPEVEEMIRDGMVGQSAVEQLAVYCYSVKKEYENLKEARKASGEVADKLRFKDSRSSK 180

RESULT 36

Db 1168 E-ABELKIRRDL---EASLQHQAQISAIRKKHQD-----ANEMADQV-----DQ 1209
 Qy 181 LQTYVSELDQAKIELSKAQDKLQS 204
 Db 1210 LQKVSKLEKDQDKDQLKREMDLSS 1233

RESULT 36

PRELIMINARY; PRT; 786 AA.

ID Q91520; AC Q91520; DT 01-NOV-1996 (TREMBUREL 01, Created)
 DT 01-NOV-1996 (TREMBUREL 01, Last sequence update)
 DE SKELETAL MYOSIN HEAVY CHAIN (FRAGMENT).
 OS Thunnus thynnus (Bluefin tuna).
 OC Actinopterygii; Neopterygii; Teleostei; Buteleosteii; Neoteleostei;
 Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
 NCBI_TAXID=837;

RN [1] SEQUENCE FROM N.A.
 RC TISSUE=FAST MUSCLE;
 RA Hitayama I., Wataoe S.;
 RT "cDNA cloning of bluefin tuna skeletal muscle myosin heavy chain."
 RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: DB5136; BA12730_1;
 DR InterPro: IPR002938; Myosin_tail.
 DR InterPro: IPR000533; tropomyosin.
 DR Pfam: PF01576; Myosin_tail; 1.
 DR PRINS; PR00194; tropomyosin.
 DR FT NON_TER 1
 SEQUENCE 786 AA; 90580 MW; 0279F714CA649A10 CRC64;

Query Match 14.7%; Score 156.5; DB 13; Length 786;
 Best Local Similarity 24.0%; Pred. No. 0.18; Mismatches 91; Indels 61; Gaps 9;
 Matches 63; Conservative 48; Mismatches 91; Indels 61; Gaps 9;

Qy 6 KLFDFLAQEEENVILDREF-----LKNELDNVRQALSQDKDEKEKRSQVID 50
 Db 23 KLRRLD--EESTIQHEATSASRKKQADSVAELGEQIDNLQRVKQLEKEKSQYKMEID 79

Qy 51 TLRLTEERNATVSLQALGKAEMLCSTLKKQMKYLQQQDTIKQQAEGAKURSKMT 110
 Db 80 DLSSNNE-----AVAKSGKNEKMCRTEDDULSELRAKNDLNGQDNLQRQIOT 132

Qy 111 -----MEQTEL- LLQSQLP-----EVEEMIRDMGVGOSAVEDLAVYCYS 148
 Db 133 ENGEFSRQEEKEKDALVSQTRGKQAYTQOEERKRHIEEKAQNHALHAVQSRHEDL 192

Qy 149 LKKEYENIKEAR-----KASEGAED--KLKDLFSSRSRKLQTVYSELDAKLELKS 197
 Db 193 LREQEYEEQEAKEGELQRMGSKANSEVAQWRTKTFETDAORTELSEAKKKLАО--RLQD 249

Qy 198 AKOKLOSAKEKMSLKKITMLO 220
 Db 250 AEESIEAVNSKCASELKWTQLO 272

RESULT 38

Q9UEE3 PRELIMINARY; PRT; 1940 AA.

ID Q9UEE3; AC Q9UEE3; DT 01-MAY-2000 (TREMBUREL 13, Created)
 DT 01-DEC-2001 (TREMBUREL 19, Last annotation update)
 DE MYOSIN HEAVY CHAIN.
 OS Pecten maximus (King scallop) (Pilgrim's clam).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;
 Pectinidae; Pecten.
 NCBI_TAXID=6579;

[1] SEQUENCE FROM N.A.
 RC TISSUE=ADDUCTOR MUSCLE;
 RA James D.P., Patel H., Chantler P.D.;
 RT "Primary structure of myosin from the striated adductor muscle of the
 Atlantic scallop, Pecten maximus";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR APF34172; ADD52842; 1; -
 DR HSSP; P24733; 1WDC
 DR InterPro: IPR000048; IQ; myosin_head.
 DR InterPro: IPR01609; myosin_head.
 DR InterPro: IPR004009; Myosin_N
 DR InterPro: IPR02928; Myosin_tail.
 DR InterPro: IPR02017; Spectrin.
 DR Pfam: PF00612; IO; 2.
 DR Pfam; PF0063; myosin_head; 1.
 DR Pfam; PF02736; Myosin_N; 1.
 DR Pfam; PF01576; Myosin_tail; 1.
 DR PRINS; PR00193; MYOSINHEAVY
 DR PRINS; PR00053; MYOSINHEAVY
 DR PRINS; PR00055; myosin_head; 1.
 DR SMART; SM00015; IQ; 1.
 DR SMART; SM00242; MSC; 1.
 DR SEQUENCE; PS50096; IQ; 1.
 OC Eukaryota; Metazoda; Chromadorea; Rhabditida; Rhabditoidea;

Query Match 14.7%; Score 156.5; DB 5; Length 1940;

Thu Sep 5 10:01:09 2002

us-09-052-089a-3.rspt

THIS PAGE BLANK (USPTO)